ABSTRACT

Variant human MLH1 and MSH2 genes are provided. Methods of using these variant genes to diagnose hereditary non-polyposis colorectal cancer (HNPCC) and/or determine a patient's susceptibility to developing HNPCC are also provided. Methods and compositions for identifying new variant MLH1 of MSH2 genes are also provided. In addition, experimental models for hereditary non-polyposis colorectal cancer comprising these variant genes are provided.